

FIGURE 1A

388	TGG	GGA	TGC	TAT	GGA	AAC	ATC	CAA	AGC	CTG	GAC	ACC	415	424	433
	W	G	C	Y	G	N	I	Q	S	L	D	T	P	G	G
442	ATT	GGA	AGA	CGT	CAC	GGC	CTG	AAC	TAC	TGT	GGA	GTT	469	478	487
	I	G	R	R	H	G	L	N	Y	C	G	V	R	A	L
496	GCT	GAA	ATA	GAC	ATG	CCA	TAC	CTC	CTG	AAA	TAT	CAA	523	532	541
	A	E	I	D	M	P	Y	L	L	K	Y	Q	P	M	I
550	GGC	CAA	AAG	TAC	TGC	ATG	GAT	CCT	GCC	GTG	ATC	GCT	577	586	595
	G	Q	K	Y	C	M	D	P	A	V	I	A	G	V	K
604	TCT	CCC	GGT	GAC	AAA	ATT	CTG	GTC	AAC	ATG	GGC	GAT	631	640	649
	S	P	G	D	K	I	L	V	N	M	G	D	R	T	Q
658	GAC	CCT	GGC	TCT	CAA	GCT	CCC	ACA	TCC	TGG	ATT	AGT	685	694	703
	D	P	G	S	Q	A	P	T	S	W	I	S	E	S	Q
712	ACA	ACT	GAA	GTT	CTG	ACT	ACT	AGA	ATC	AAA	GAA	ATC	739	748	757
	T	T	E	V	L	T	T	R	I	K	E	I	Q	R	T

FIGURE 1B

766	775	784	793	802	811
TGG ACC CCT GAC CAG TAC CTG AGA GGT GGA CTC TGT GCC TAC AGT GGG GGT GCT					
W T P D Q Y L R G G L C A Y S G A					
820	829	838	847	856	865
GGC TAT GTC CGA AGC AGC CAG GAC CTG AGC TGT GAC TTC TGC AAT GAT GTC CTT					
G Y V R S S Q D L S C D F C N D V L					
874	883	892	901	910	919
GCA CGA GCC AAG TAC CTC AAG AGA CAT GGC TTC TAA CAT CTC AGA TGA AAC CCA					
A R A K Y L K R H G F					
928	937	946	955	964	973
AGA CCA TGA TCA CAT ATG CAG CAG CCT CAA ATG TTA CAC AGA TAA AAC TAG CCA AGG					
982	991	1000	1009	1018	1027
GCA CCT GTA ACT GGG AAT CTG AGT TTG ACC TAA AAG TCA TTA AAA TAA CAT GAA					
1036	1045				
TCA CAT TAA AGG AAG AAT T 3'					

FIGURE 1C

1	MSA	- - - - -	LWLLGLLALMDLSESSNW	G	2372794
1	MLGKNDP	MC	LVLLGLTAL	LGICQGGT -	GI 63428
24	CYGNIQSL	DT	PGASCGIGRRHGL	NYCGVRA	2372794
30	CYGSVSR	IDT	TGASCR	TAKPEGLSYCGVRA	GI 63428
54	SERLAEI	DM	PYLLKYQPMMQT	IGQKYCMDP	2372794
60	SRTIAER	D	LGSMNKYKVL	IKRVGEALCIEP	GI 63428
84	AVIAGVLS	RKSPGDK	ILVNM	- GDRTS -	2372794
90	AVIAGI	ISRES	HAGKIL	KNGWGDRGN	GI 63428
109	-MVQDPGS	QAP	TSWIS	ESQVSQTTEVLTTR	2372794
120	MQVDKRY	HKIEGT	WNGE	AHIRQGT	ILIDM
138	IK	EIQRRFP	TWTP	DDQYL	RGGLCAYSGAGY
150	VKKIQ	KFP	WR	DDQQL	KGGISAYNAGVGN
168	VRS	SQDLSC	- - - - -	DFCNDV	LARAKYLKRH
180	VRSY	ERM	DIG	TLD	DYSNDVVARAQYFKQH
193	GF				2372794
210	GY				GI 63428

FIGURE 2